

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HU, JING-SHAN
ROSEN, CRAIG A.
CAO, LIANG
- (ii) TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 - (B) STREET: 1100 NEW YORK AVENUE
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: TO BE ASSIGNED
 - (B) FILING DATE: HERewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/207,550
 - (B) FILING DATE: 8-MAR-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/465,968
 - (B) FILING DATE: 06-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MARKOWICZ, KAREN R.
 - (B) REGISTRATION NUMBER: 36,351
 - (C) REFERENCE/DOCKET NUMBER: 1488.1000004
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)371-2600
 - (B) TELEFAX: (202)371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1674 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 12..80

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 81..1268

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..1268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|--|-----|
| GTCCTTCCAC C ATG CAC TCG CTG GGC TTC TTC TCT GTG GCG TGT TCT CTG | 50 |
| Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu | |
| -23 -20 -15 | |
| CTC GCC GCT GCG CTG CTC CCG GGT CCT CGC GAG GCG CCC GCC GCC GCC | 98 |
| Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala | |
| -10 -5 1 5 | |
| GCC GCC TTC GAG TCC GGA CTC GAC CTC TCG GAC GCG GAG CCC GAC GCG | 146 |
| Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala | |
| 10 15 20 | |
| GGC GAG GCC ACG GCT TAT GCA AGC AAA GAT CTG GAG GAG CAG TTA CGG | 194 |
| Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg | |
| 25 30 35 | |
| TCT GTG TCC AGT GTA GAT GAA CTC ATG ACT GTA CTC TAC CCA GAA TAT | 242 |
| Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr | |
| 40 45 50 | |
| TGG AAA ATG TAC AAG TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC | 290 |
| Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn | |
| 55 60 65 70 | |
| AGA GAA CAG GCC AAC CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT | 338 |
| Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe | |
| 75 80 85 | |
| GCT GCA GCA CAT TAT AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG | 386 |
| Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu | |
| 90 95 100 | |
| TGG AGA AAG ACT CAA TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG | 434 |
| Trp Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly | |
| 105 110 115 | |
| AAG GAG TTT GGA GTC GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG | 482 |
| Lys Glu Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val | |
| 120 125 130 | |
| TCC GTC TAC AGA TGT GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC | 530 |
| Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys | |
| 135 140 145 150 | |

| | |
|---|------|
| ATG AAC ACC AGC ACG AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr 155 160 165 | 578 |
| GTG CCT CTC TCT CAA GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn 170 175 180 | 626 |
| CAC ACT TCC TGC CGA TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val 185 190 195 | 674 |
| CAT TCC ATT ATT AGA CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln 200 205 210 | 722 |
| GCA GCG AAC AAG ACC TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile 215 220 225 230 | 770 |
| TGC AGA TGC CTG GCT CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly 235 240 245 | 818 |
| GAT GAC TCA ACA GAT GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu 250 255 260 | 866 |
| CTG GAT GAA GAG ACC TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro 265 270 275 | 914 |
| GCC AGC TGT GGA CCC CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys 280 285 290 | 962 |
| GTC TGT AAA AAC AAA CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu 295 300 305 310 | 1010 |
| TTT GAT GAA AAC ACA TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg 315 320 325 | 1058 |
| AAT CAA CCC CTA AAT CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser 330 335 340 | 1106 |
| CCA CAG AAA TGC TTG TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys 345 350 355 | 1154 |
| AGC TGT TAC AGA CGG CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro 360 365 370 | 1202 |
| GGA TTT TCA TAT AGT GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp 375 380 385 390 | 1250 |
| CAA AGA CCA CAA ATG AGC TAAGATTGTA CTGTTTTCCTA GTTCATCGAT | 1298 |

Gln Arg Pro Gln Met Ser
395

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| TTTCTATTAT | GGAAACTGT | GTTGCCACAG | TAGAACTGTC | TGTGAACAGA | GAGACCCTTG | 1358 |
| TGGGTCCATG | CTAACAAAGA | CAAAAGTCTG | TCTTTCCTGA | ACCATGTGGA | TAACCTTTACA | 1418 |
| GAAATGGACT | GGAGCTCATC | TGCAAAAGGC | CTCTTGTAAG | GACTGGTTTT | CTGCCAATGA | 1478 |
| CCAAACAGCC | AAGATTTTCC | TCTTGTGATT | TCTTTAAAG | AATGACTATA | TAATTTATTT | 1538 |
| CCACTAAAAA | TATTGTTTCT | GCATTCATTT | TTATAGCAAC | AACAATTGGT | AAAACCTACT | 1598 |
| GTGATCAATA | TTTTTATATC | ATGCAAAATA | TGTTTAAAT | AAAATGAAAA | TTGTATTAT | 1658 |
| AAAAAAAAAA | AAAAAA | | | | | 1674 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Ser | Leu | Gly | Phe | Phe | Ser | Val | Ala | Cys | Ser | Leu | Leu | Ala | Ala | |
| -23 | | | -20 | | | | | -15 | | | | | -10 | | | |
| Ala | Leu | Leu | Pro | Gly | Pro | Arg | Glu | Ala | Pro | Ala | Ala | Ala | Ala | Ala | Phe | |
| | | -5 | | | | | 1 | | | | 5 | | | | | |
| Glu | Ser | Gly | Leu | Asp | Leu | Ser | Asp | Ala | Glu | Pro | Asp | Ala | Gly | Glu | Ala | |
| 10 | | | | 15 | | | | | | 20 | | | | 25 | | |
| Thr | Ala | Tyr | Ala | Ser | Lys | Asp | Leu | Glu | Gln | Leu | Arg | Ser | Val | Ser | | |
| | | | | 30 | | | | 35 | | | | | 40 | | | |
| Ser | Val | Asp | Glu | Leu | Met | Thr | Val | Leu | Tyr | Pro | Glu | Tyr | Trp | Lys | Met | |
| | | 45 | | | | | | 50 | | | | | 55 | | | |
| Tyr | Lys | Cys | Gln | Leu | Arg | Lys | Gly | Gly | Trp | Gln | His | Asn | Arg | Glu | Gln | |
| | | 60 | | | | | 65 | | | | | 70 | | | | |
| Ala | Asn | Leu | Asn | Ser | Arg | Thr | Glu | Glu | Thr | Ile | Lys | Phe | Ala | Ala | Ala | |
| | 75 | | | | | 80 | | | | | 85 | | | | | |
| His | Tyr | Asn | Thr | Glu | Ile | Leu | Lys | Ser | Ile | Asp | Asn | Glu | Trp | Arg | Lys | |
| 90 | | | | | 95 | | | | 100 | | | | | | 105 | |
| Thr | Gln | Cys | Met | Pro | Arg | Glu | Val | Cys | Ile | Asp | Val | Gly | Lys | Glu | Phe | |
| | | | 110 | | | | | 115 | | | | | | 120 | | |
| Gly | Val | Ala | Thr | Asn | Thr | Phe | Phe | Lys | Pro | Pro | Cys | Val | Ser | Val | Tyr | |
| | | 125 | | | | | | 130 | | | | | 135 | | | |
| Arg | Cys | Gly | Gly | Cys | Cys | Asn | Ser | Glu | Gly | Leu | Gln | Cys | Met | Asn | Thr | |
| | | 140 | | | | | 145 | | | | | 150 | | | | |

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
155 160 165

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
170 175 180 185

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
190 195 200

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
205 210 215

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
220 225 230

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
235 240 245

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
250 255 260 265

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
270 275 280

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
285 290 295

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
300 305 310

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
315 320 325

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
330 335 340 345

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
350 355 360

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
365 370 375

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro
380 385 390

Gln Met Ser
395

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide

(B) LOCATION: 71..142

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 143..1120

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 71..1120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| CGAGGCCACG GCTTATGCAA GCAAAGATCT GGAGGAGCAG TTACGGTCTG TGTCCAGTGT | 60 |
| AGATGAACTC ATG ACT GTA CTC TAC CCA GAA TAT TGG AAA ATG TAC AAG | 109 |
| Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys | |
| -24 -20 -15 | |
| TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC AGA GAA CAG GCC AAC | 157 |
| Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn | |
| -10 -5 1 5 | |
| CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT GCT GCA GCA CAT TAT | 205 |
| Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr | |
| 10 15 20 | |
| AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG TGG AGA AAG ACT CAA | 253 |
| Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln | |
| 25 30 35 | |
| TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG AAG GAG TTT GGA GTC | 301 |
| Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val | |
| 40 45 50 | |
| GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG TCC GTC TAC AGA TGT | 349 |
| Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys | |
| 55 60 65 | |
| GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC ATG AAC ACC AGC ACG | 397 |
| Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr | |
| 70 75 80 85 | |
| AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA GTG CCT CTC TCT CAA | 445 |
| Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln | |
| 90 95 100 | |
| GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT CAC ACT TCC TGC CGA | 493 |
| Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg | |
| 105 110 115 | |
| TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT CAT TCC ATT ATT AGA | 541 |
| Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg | |
| 120 125 130 | |
| CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG GCA GCG AAC AAG ACC | 589 |
| Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr | |
| 135 140 145 | |
| TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC TGC AGA TGC CTG GCT | 637 |
| Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala | |

| | | | | | | | |
|---|--|-----|--|-----|--|-----|------|
| 150 | | 155 | | 160 | | 165 | |
| CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA GAT GAC TCA ACA GAT | | | | | | | 685 |
| Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp | | | | | | | |
| | | 170 | | 175 | | 180 | |
| GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG CTG GAT GAA GAG ACC | | | | | | | 733 |
| Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr | | | | | | | |
| | | 185 | | 190 | | 195 | |
| TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT GCC AGC TGT GGA CCC | | | | | | | 781 |
| Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro | | | | | | | |
| | | 200 | | 205 | | 210 | |
| CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT GTC TGT AAA AAC AAA | | | | | | | 829 |
| His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys | | | | | | | |
| | | 215 | | 220 | | 225 | |
| CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA TTT GAT GAA AAC ACA | | | | | | | 877 |
| Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr | | | | | | | |
| | | 230 | | 235 | | 240 | 245 |
| TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA AAT CAA CCC CTA AAT | | | | | | | 925 |
| Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn | | | | | | | |
| | | 250 | | 255 | | 260 | |
| CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT CCA CAG AAA TGC TTG | | | | | | | 973 |
| Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu | | | | | | | |
| | | 265 | | 270 | | 275 | |
| TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC AGC TGT TAC AGA CGG | | | | | | | 1021 |
| Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg | | | | | | | |
| | | 280 | | 285 | | 290 | |
| CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA GGA TTT TCA TAT AGT | | | | | | | 1069 |
| Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser | | | | | | | |
| | | 295 | | 300 | | 305 | |
| GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG CAA AGA CCA CAA ATG | | | | | | | 1117 |
| Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met | | | | | | | |
| | | 310 | | 315 | | 320 | 325 |
| AGC TAAGATTGTA CTGTTTCCCA GTTCATCGAT TTTCTATTAT GGAAAACTGT | | | | | | | 1170 |
| Ser | | | | | | | |
| GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG TGGGTCCATG CTAACAAAGA | | | | | | | 1230 |
| CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA GAAATGGACT GGAGCTCATC | | | | | | | 1290 |
| TGCAAAAGGC CTCTTGTAAG GACTGGTTTT CTGCCAATGA CCAAACAGCC AAGATTTTCC | | | | | | | 1350 |
| TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT CCACTAAAAA TATTGTTTCT | | | | | | | 1410 |
| GCATTCATTT TTATAGCAAC AACAATTGGT AAAACTCACT GTGATCAATA TTTTATATC | | | | | | | 1470 |
| ATGCAAAATA TGTTTAAAAT AAAATGAAAA TTGTATTTAT AAAAAAAAAA AAAAAA | | | | | | | 1526 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Leu | Tyr | Pro | Glu | Tyr | Trp | Lys | Met | Tyr | Lys | Cys | Gln | Leu | -24 | -20 | -15 | -10 |
| Arg | Lys | Gly | Gly | Trp | Gln | His | Asn | Arg | Glu | Gln | Ala | Asn | Leu | Asn | Ser | -5 | 1 | 5 | |
| Arg | Thr | Glu | Glu | Thr | Ile | Lys | Phe | Ala | Ala | Ala | His | Tyr | Asn | Thr | Glu | 10 | 15 | 20 | |
| Ile | Leu | Lys | Ser | Ile | Asp | Asn | Glu | Trp | Arg | Lys | Thr | Gln | Cys | Met | Pro | 25 | 30 | 35 | 40 |
| Arg | Glu | Val | Cys | Ile | Asp | Val | Gly | Lys | Glu | Phe | Gly | Val | Ala | Thr | Asn | 45 | 50 | 55 | |
| Thr | Phe | Phe | Lys | Pro | Pro | Cys | Val | Ser | Val | Tyr | Arg | Cys | Gly | Gly | Cys | 60 | 65 | 70 | |
| Cys | Asn | Ser | Glu | Gly | Leu | Gln | Cys | Met | Asn | Thr | Ser | Thr | Ser | Tyr | Leu | 75 | 80 | 85 | |
| Ser | Lys | Thr | Leu | Phe | Glu | Ile | Thr | Val | Pro | Leu | Ser | Gln | Gly | Pro | Lys | 90 | 95 | 100 | |
| Pro | Val | Thr | Ile | Ser | Phe | Ala | Asn | His | Thr | Ser | Cys | Arg | Cys | Met | Ser | 105 | 110 | 115 | 120 |
| Lys | Leu | Asp | Val | Tyr | Arg | Gln | Val | His | Ser | Ile | Ile | Arg | Arg | Ser | Leu | 125 | 130 | 135 | |
| Pro | Ala | Thr | Leu | Pro | Gln | Cys | Gln | Ala | Ala | Asn | Lys | Thr | Cys | Pro | Thr | 140 | 145 | 150 | |
| Asn | Tyr | Met | Trp | Asn | Asn | His | Ile | Cys | Arg | Cys | Leu | Ala | Gln | Glu | Asp | 155 | 160 | 165 | |
| Phe | Met | Phe | Ser | Ser | Asp | Ala | Gly | Asp | Asp | Ser | Thr | Asp | Gly | Phe | His | 170 | 175 | 180 | |
| Asp | Ile | Cys | Gly | Pro | Asn | Lys | Glu | Leu | Asp | Glu | Glu | Thr | Cys | Gln | Cys | 185 | 190 | 195 | 200 |
| Val | Cys | Arg | Ala | Gly | Leu | Arg | Pro | Ala | Ser | Cys | Gly | Pro | His | Lys | Glu | 205 | 210 | 215 | |
| Leu | Asp | Arg | Asn | Ser | Cys | Gln | Cys | Val | Cys | Lys | Asn | Lys | Leu | Phe | Pro | 220 | 225 | 230 | |
| Ser | Gln | Cys | Gly | Ala | Asn | Arg | Glu | Phe | Asp | Glu | Asn | Thr | Cys | Gln | Cys | 235 | 240 | 245 | |
| Val | Cys | Lys | Arg | Thr | Cys | Pro | Arg | Asn | Gln | Pro | Leu | Asn | Pro | Gly | Lys | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 250 | | 255 | | 260 | | | | | | | | | | | |
| Cys | Ala | Cys | Glu | Cys | Thr | Glu | Ser | Pro | Gln | Lys | Cys | Leu | Leu | Lys | Gly |
| 265 | | | | | 270 | | | | | 275 | | | | | 280 |
| Lys | Lys | Phe | His | His | Gln | Thr | Cys | Ser | Cys | Tyr | Arg | Arg | Pro | Cys | Thr |
| | | | 285 | | | | | | 290 | | | | | 295 | |
| Asn | Arg | Gln | Lys | Ala | Cys | Glu | Pro | Gly | Phe | Ser | Tyr | Ser | Glu | Glu | Val |
| | | 300 | | | | | | 305 | | | | | 310 | | |
| Cys | Arg | Cys | Val | Pro | Ser | Tyr | Trp | Gln | Arg | Pro | Gln | Met | Ser | | |
| | | 315 | | | | | 320 | | | | | 325 | | | |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Thr | Leu | Ala | Cys | Leu | Leu | Leu | Leu | Gly | Cys | Gly | Tyr | Leu | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| His | Val | Leu | Ala | Glu | Glu | Ala | Glu | Ile | Pro | Arg | Glu | Val | Ile | Glu | Arg |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Leu | Ala | Arg | Ser | Gln | Ile | His | Ser | Ile | Arg | Asp | Leu | Gln | Arg | Leu | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Ile | Asp | Ser | Val | Gly | Ser | Glu | Asp | Ser | Leu | Asp | Thr | Ser | Leu | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | His | Gly | Val | His | Ala | Thr | Lys | His | Val | Pro | Glu | Lys | Arg | Pro | Leu |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 |
| Pro | Ile | Arg | Arg | Lys | Arg | Ser | Ile | Glu | Glu | Ala | Val | Pro | Ala | Val | Cys |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Lys | Thr | Arg | Thr | Val | Ile | Tyr | Glu | Ile | Pro | Arg | Ser | Gln | Val | Asp | Pro |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Thr | Ser | Ala | Asn | Phe | Leu | Ile | Trp | Pro | Pro | Cys | Val | Glu | Val | Lys | Arg |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Cys | Thr | Gly | Cys | Cys | Asn | Thr | Ser | Ser | Val | Lys | Cys | Gln | Pro | Ser | Arg |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | His | His | Arg | Ser | Val | Lys | Val | Ala | Lys | Val | Glu | Tyr | Val | Arg | Lys |
| 145 | | | | 150 | | | | | 155 | | | | | | 160 |
| Lys | Pro | Lys | Leu | Lys | Glu | Val | Gln | Val | Arg | Leu | Glu | Glu | His | Leu | Glu |
| | | | 165 | | | | | 170 | | | | | | 175 | |

Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
180 185 190

Thr Asp Val Arg
195

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Arg | Cys | Trp | Ala | Leu | Phe | Leu | Ser | Leu | Cys | Cys | Tyr | Leu | Arg | 1 | 5 | 10 | 15 |
| Leu | Val | Ser | Ala | Glu | Gly | Asp | Pro | Ile | Pro | Glu | Glu | Leu | Tyr | Glu | Met | 20 | 25 | 30 | |
| Leu | Ser | Asp | His | Ser | Ile | Arg | Ser | Phe | Asp | Asp | Leu | Gln | Arg | Leu | Leu | 35 | 40 | 45 | |
| His | Gly | Asp | Pro | Gly | Glu | Glu | Asp | Gly | Ala | Glu | Leu | Asp | Leu | Asn | Met | 50 | 55 | 60 | |
| Thr | Arg | Ser | His | Ser | Gly | Gly | Glu | Leu | Glu | Ser | Leu | Ala | Arg | Gly | Arg | 65 | 70 | 75 | 80 |
| Arg | Ser | Leu | Gly | Ser | Leu | Thr | Ile | Ala | Glu | Pro | Ala | Met | Ile | Ala | Glu | 85 | 90 | 95 | |
| Cys | Lys | Thr | Arg | Thr | Glu | Val | Phe | Glu | Ile | Ser | Arg | Arg | Leu | Ile | Asp | 100 | 105 | 110 | |
| Arg | Thr | Asn | Ala | Asn | Phe | Leu | Val | Trp | Pro | Pro | Cys | Val | Glu | Val | Gln | 115 | 120 | 125 | |
| Arg | Cys | Ser | Gly | Cys | Cys | Asn | Asn | Arg | Asn | Val | Gln | Cys | Arg | Pro | Thr | 130 | 135 | 140 | |
| Gln | Val | Gln | Leu | Arg | Pro | Val | Gln | Val | Arg | Lys | Ile | Glu | Ile | Val | Arg | 145 | 150 | 155 | 160 |
| Lys | Lys | Pro | Ile | Phe | Lys | Lys | Ala | Thr | Val | Thr | Leu | Glu | Asp | His | Leu | 165 | 170 | 175 | |
| Ala | Cys | Lys | Cys | Glu | Thr | Val | Ala | Ala | Ala | Arg | Pro | Val | Thr | Arg | Ser | 180 | 185 | 190 | |
| Pro | Gly | Gly | Ser | Gln | Glu | Gln | Arg | Ala | Lys | Thr | Pro | Gln | Thr | Arg | Val | 195 | 200 | 205 | |
| Thr | Ile | Arg | Thr | Val | Arg | Val | Arg | Arg | Pro | Pro | Lys | Gly | Lys | His | Arg | | | | |

| | | | | |
|---|--|-----|--|-----|
| 210 | | 215 | | 220 |
| Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly | | | | |
| 225 | | 230 | | 235 |
| Ala | | | | 240 |

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Phe | Leu | Leu | Ser | Trp | Val | His | Trp | Ser | Leu | Ala | Leu | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Tyr | Leu | His | His | Ala | Lys | Trp | Ser | Gln | Ala | Ala | Pro | Met | Ala | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Gly | Gln | Asn | His | His | Glu | Val | Val | Lys | Phe | Met | Asp | Val | Tyr | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Ser | Tyr | Cys | His | Pro | Ile | Glu | Thr | Leu | Val | Asp | Ile | Phe | Gln | Glu |
| 50 | | | | | | 55 | | | | | 60 | | | | |
| Tyr | Pro | Asp | Glu | Ile | Glu | Tyr | Ile | Phe | Lys | Pro | Ser | Cys | Val | Pro | Leu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Met | Arg | Cys | Gly | Gly | Cys | Cys | Asn | Asp | Glu | Gly | Leu | Glu | Cys | Val | Pro |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Thr | Glu | Glu | Ser | Asn | Ile | Thr | Met | Gln | Ile | Met | Arg | Ile | Lys | Pro | His |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gln | Gly | Gln | His | Ile | Gly | Glu | Met | Ser | Phe | Leu | Gln | His | Asn | Lys | Cys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Glu | Cys | Arg | Pro | Lys | Lys | Asp | Arg | Ala | Arg | Gln | Glu | Lys | Lys | Ser | Val |
| 130 | | | | | | 135 | | | | | 140 | | | | |
| Arg | Gly | Lys | Gly | Lys | Gly | Gln | Lys | Arg | Lys | Arg | Lys | Lys | Ser | Arg | Tyr |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Lys | Ser | Trp | Ser | Val | Tyr | Val | Gly | Ala | Arg | Cys | Cys | Leu | Met | Pro | Trp |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ser | Leu | Pro | Gly | Pro | His | Pro | Cys | Gly | Pro | Cys | Ser | Glu | Arg | Arg | Lys |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| His | Leu | Phe | Val | Gln | Asp | Pro | Gln | Thr | Cys | Lys | Cys | Ser | Cys | Lys | Asn |
| | | 195 | | | | | 200 | | | | | | 205 | | |

Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr
210 215 220

Cys Arg Cys Asp Lys Pro Arg Arg
225 230

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGCTTCCGG CTCGTATG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTTTTCCC AGTCACGAC

18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACATGGTT CAGGAAAGAC A

21

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTAATACGA CTCACTATAG GGATCCCGCC ATGGAGGCCA CGGCTTATGC

50

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCTCTAGA TTAGCTCATT TGTGGTCT

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGATCCA TGACTGTACT CTACCCA

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAC TCGAGGCTCA TTTGTGGTCT

60

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAC TCGAGGCTCA TTTGTGGTCT